

In the Claims

Please amend claims 1-13, 26-34, 43-44 and 63 as follows:

1. (currently amended) A composition comprising a ~~substantially~~ purified mannanase A peptide, the mannanase A peptide comprising a catalytic domain glycoside hydrolase family 5 (GH5), a carbohydrate binding domain III, and a carbohydrate binding domain II in that order.
2. (currently amended) The composition of claim 1 wherein the mannanase A peptide is ~~further defined as comprising a~~ comprises linker sequences connecting the catalytic domain GH5, the carbohydrate binding domain III, and the carbohydrate binding domain II; and a signal peptide.
3. (currently amended) The composition of claim 1 ~~or 2~~ wherein the ~~first~~ catalytic domain GH5 of the mannanase A peptide is further defined as having a length of about 370 to about 380 amino acids.
4. (currently amended) The composition of claim 1, ~~2, or 3,~~ wherein the carbohydrate binding domain III of the mannanase A peptide is further defined as having a length of about 140 to about 160 amino acids.
5. (currently amended) The composition of claim 1, or 2, 3, ~~or 4~~ wherein the carbohydrate binding domain II of the mannanase A peptide is further defined as having a length of about 90 amino acids to about 110 amino acids in length.
6. (original) The composition of claim 3 wherein the GH5 catalytic domain is further defined as the sequence of SEQ ID NO: 3.

7. (currently amended) The composition of claim 4-1 wherein the carbohydrate binding domain III is further defined as the sequence of SEQ ID NO: 4.

8. (currently amended) The composition of claim 5-1 wherein the carbohydrate binding domain II is further defined as the sequence of SEQ ID NO: 5.

9. (currently amended) The composition of claim 1 further defined as comprising a sequence of SEQ ID NO. 3, wherein the carbohydrate binding domain III has a sequence of SEQ ID NO: 4, and the carbohydrate binding domain II has a sequence of SEQ ID NO: 5.

10. (currently amended) A purified mannanase A peptide having a sequence of SEQ ID NO: 1.

11. (currently amended) The purified mannanase A peptide of claim 10 further defined as having its encoding nucleotide sequence the same as a sequence of SEQ ID NO: 2.

12. (currently amended) An industrial detergent mixture suitable for degrading hemicellulose, such mixture comprising the mannanase A of claim 1.

13. (cancelled) The industrial mixture of claim 12 further defined as comprising a detergent.

14-25. (previously cancelled)

26. (currently amended) An isolated polypeptide molecule capable of degrading mannose comprising:

a) a sequence of SEQ ID NO: 3; SEQ ID NO: 4 and SEQ ID NO: 5 in that order,

or,

~~b) a sequence of SEQ ID NO: 4;~~

~~c) a sequence of SEQ ID NO: 5;~~

~~d) b) a sequence of SEQ ID NO: 1; or~~

~~e) c) a SEQ ID NO: 2; or~~

~~f) d) an amino acid sequence having at least 70% sequence identity with the amino acid sequence of a); or b), ~~c)~~, ~~or d)~~.~~

27. (currently amended) The polypeptide molecule of claim 26, having at least 90% sequence identity with the amino acid sequence of a); or b), ~~c)~~, ~~or d)~~.

28. (original) A fusion protein comprising the polypeptide of claim 26 and a heterologous peptide.

29. (original) The fusion protein of claim 28, wherein the heterologous peptide is a substrate targeting moiety.

30. (original) The fusion protein of claim 29, wherein the heterologous peptide is a peptide tag.

31. (currently amended) The fusion protein of claim 29, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, GST gene specific tag, or OmpA signal sequence tag.

32. (original) The fusion protein of claim 29, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

33. (original) The fusion protein of claim 32, wherein the agent is a leucine zipper.